

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/008,264B
Source: 1FW/6
Date Processed by STIC: 7/29/05

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
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U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05



IFW16

RAW SEQUENCE LISTING

DATE: 07/29/2005

PATENT APPLICATION: US/10/008,264B

TIME: 08:03:58

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\07292005\J008264B.raw

3 <110> APPLICANT: Glimcher, Laurie H.
 4 Szabo, Susanne, J.
 6 <120> TITLE OF INVENTION: T-BET COMPOSITIONS AND METHODS OF USE THEREOF
 8 <130> FILE REFERENCE: HUI-040CP
 10 <140> CURRENT APPLICATION NUMBER: US 10/008264B
 11 <141> CURRENT FILING DATE: 2001-12-03
 13 <150> PRIOR APPLICATION NUMBER: PCT/US00/15345
 14 <151> PRIOR FILING DATE: 2000-06-01
 16 <150> PRIOR APPLICATION NUMBER: US 60/137085
 17 <151> PRIOR FILING DATE: 1999-06-02
 19 <160> NUMBER OF SEQ ID NOS: 9
 21 <170> SOFTWARE: PatentIn Ver. 2.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1608
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(1605)
 32 <400> SEQUENCE: 1
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 35 1 5 10 15
 37 ccg atg ccg ggg agc gac gag ggc ccg gcg cct ggc gcc gac ccg cag 96
 38 Pro Met Pro Gly Ser Asp Glu Gly Arg Ala Pro Gly Ala Asp Pro Gln
 39 20 25 30
 41 cac cgc tac ttc tac ccg gag ccg ggc gcg cag gac gcg gac gag cgt 144
 42 His Arg Tyr Phe Tyr Pro Glu Pro Gly Ala Gln Asp Ala Asp Glu Arg
 43 35 40 45
 45 cgc ggg ggc ggc agc ctg ggg tct ccc tac ccg ggg ggc gcc ttg gtg 192
 46 Arg Gly Gly Gly Ser Leu Gly Ser Pro Tyr Pro Gly Gly Ala Leu Val
 47 50 55 60
 49 ccc gcc ccg ccg agc cgc ttc ctt gga gcc tac gcc tac ccg ccg cga 240
 50 Pro Ala Pro Pro Ser Arg Phe Leu Gly Ala Tyr Ala Tyr Pro Pro Arg
 51 65 70 75 80
 53 ccc cag gcg gcc ggc ttc ccc ggc gcg ggc gag tcc ttc ccg ccg ccc 288
 54 Pro Gln Ala Ala Gly Phe Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro
 55 85 90 95
 57 gcg gac gcc gag ggc tac cag ccg ggc gag ggc tac gcc gcc ccg gac 336
 58 Ala Asp Ala Glu Gly Tyr Gln Pro Gly Glu Gly Tyr Ala Ala Pro Asp
 59 100 105 110
 62 ccg cgc gcc ggg ctc tac ccg ggg ccg cgt gag gac tac gcg cta ccc 384
 63 Pro Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro

Does Not Comply
 Corrected Diskette Needed

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Input Set : A:\SEQUENCE LISTING.txt

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64	115	120	125	
66	gcg gga ctg gag gtg tgc ggg aaa ctg agg gtc gcg ctc aac aac cac	432		
67	Ala Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Asn Asn His			
68	130	135	140	
70	ctg ttg tgg tcc aag ttt aat cag cac cag aca gag atg atc atc acc	480		
71	Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr			
72	145	150	155	160
74	aag cag gga cgg cgg atg ttc cca ttc ctg tca ttt act gtg gcc ggg	528		
75	Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly			
76	165	170	175	
78	ctg gag ccc acc agc cac tac agg atg ttt gtg gac gtg gtc ttg gtg	576		
79	Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val			
80	180	185	190	
82	gac cag cac cac tgg cgg tac cag agc ggc aag tgg gtg cag tgt gga	624		
83	Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly			
84	195	200	205	
86	aag gcc gag ggc agc atg cca gga aac cgc ctg tac gtc cac ccg gac	672		
87	Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp			
88	210	215	220	
90	tcc ccc aac aca gga gcg cac tgg atg cgc cag gaa gtt tca ttt ggg	720		
91	Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly			
92	225	230	235	240
94	aaa cta aag ctc aca aac aac aag ggg gcg tcc aac aat gtg acc cag	768		
95	Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln			
96	245	250	255	
98	atg att gtg ctc cag tcc ctc cat aag tac cag ccc cgg ctg cat atc	816		
99	Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile			
100	260	265	270	
102	gtt gag gtg aac gac gga gag cca gag gca gcc tgc aac gct tcc aac	864		
103	Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn			
104	275	280	285	
106	acg cat atc ttt act ttc caa gaa acc cag ttc att gcc gtg act gcc	912		
107	Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala			
108	290	295	300	
110	tac cag aat gcc gag att act cag ctg aaa att gat aat aac ccc ttt	960		
111	Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe			
112	305	310	315	320
114	gcc aaa gga ttc cgg gag aac ttt gag tcc atg tac aca tct gtt gac	1008		
115	Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp			
116	325	330	335	
118	acc agc atc ccc tcc ccg cct gga ccc aac tgt caa ttc ctt ggg gga	1056		
119	Thr Ser Ile Pro Ser Pro Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly			
120	340	345	350	
123	gat cac tac tct cct ctc cta ccc aac cag tat cct gtt ccc agc cgc	1104		
124	Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg			
125	355	360	365	
127	ttc tac ccc gac ctt cct ggc cag gcg aag gat gtg gtt ccc cag gct	1152		
128	Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala			
129	370	375	380	

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\07292005\J008264B.raw

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131 tac tgg ctg ggg gcc ccc cgg gac cac agc tat gag gct gag ttt cga 1200
132 Tyr Trp Leu Gly Ala Pro Arg Asp His Ser Tyr Glu Ala Glu Phe Arg
133 385 390 395 400
135 gca gtc agc atg aag cct gca ttc ttg ccc tct gcc cct ggg ccc acc 1248
136 Ala Val Ser Met Lys Pro Ala Phe Leu Pro Ser Ala Pro Gly Pro Thr
137 405 410 415
139 atg tcc tac tac cga ggc cag gag gtc ctg gca cct gga gct ggc tgg 1296
140 Met Ser Tyr Tyr Arg Gly Gln Glu Val Leu Ala Pro Gly Ala Gly Trp
141 420 425 430
143 cct gtg gca ccc cag tac cct ccc aag atg ggc ccg gcc agc tgg ttc 1344
144 Pro Val Ala Pro Gln Tyr Pro Pro Lys Met Gly Pro Ala Ser Trp Phe
145 435 440 445
147 cgc cct atg cgg act ctg ccc atg gaa ccc ggc cct gga ggc tca gag 1392
148 Arg Pro Met Arg Thr Leu Pro Met Glu Pro Gly Pro Gly Gly Ser Glu
149 450 455 460
151 gga cgg gga cca gag gac cag ggt ccc ccc ttg gtg tgg act gag att 1440
152 Gly Arg Gly Pro Glu Asp Gln Gly Pro Pro Leu Val Trp Thr Glu Ile
153 465 470 475 480
155 gcc ccc atc cgg ccg gaa tcc agt gat tca gga ctg ggc gaa gga gac 1488
156 Ala Pro Ile Arg Pro Glu Ser Ser Asp Ser Gly Leu Gly Glu Gly Asp
157 485 490 495
159 tct aag agg agg cgc gtg tcc ccc tat cct tcc agt ggt gac agc tcc 1536
160 Ser Lys Arg Arg Arg Val Ser Pro Tyr Pro Ser Ser Gly Asp Ser Ser
161 500 505 510
163 tcc cct gct ggg gcc cct tct cct ttt gat aag gaa gct gaa gga cag 1584
164 Ser Pro Ala Gly Ala Pro Ser Pro Phe Asp Lys Glu Ala Glu Gly Gln
165 515 520 525
167 ttt tat aac tat ttt ccc aac tga 1608
168 Phe Tyr Asn Tyr Phe Pro Asn
169 530 535
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 535
174 <212> TYPE: PRT
175 <213> ORGANISM: Homo sapiens
177 <400> SEQUENCE: 2
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181 Pro Met Pro Gly Ser Asp Glu Gly Arg Ala Pro Gly Ala Asp Pro Gln
182 20 25 30
184 His Arg Tyr Phe Tyr Pro Glu Pro Gly Ala Gln Asp Ala Asp Glu Arg
185 35 40 45
187 Arg Gly Gly Gly Ser Leu Gly Ser Pro Tyr Pro Gly Gly Ala Leu Val
188 50 55 60
190 Pro Ala Pro Pro Ser Arg Phe Leu Gly Ala Tyr Ala Tyr Pro Pro Arg
191 65 70 75 80
193 Pro Gln Ala Ala Gly Phe Pro Gly Ala Gly Glu Ser Phe Pro Pro Pro
194 85 90 95
196 Ala Asp Ala Glu Gly Tyr Gln Pro Gly Glu Gly Tyr Ala Ala Pro Asp
197 100 105 110

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DATE: 07/29/2005

PATENT APPLICATION: US/10/008,264B

TIME: 08:03:58

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\07292005\J008264B.raw

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199 Pro Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro
200      115      120      125
202 Ala Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Asn Asn His
203      130      135      140
205 Leu Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr
206 145      150      155      160
208 Lys Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly
209      165      170      175
211 Leu Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val
212      180      185      190
214 Asp Gln His His Trp Arg Tyr Gln Ser Gly Lys Trp Val Gln Cys Gly
215      195      200      205
217 Lys Ala Glu Gly Ser Met Pro Gly Asn Arg Leu Tyr Val His Pro Asp
218      210      215      220
220 Ser Pro Asn Thr Gly Ala His Trp Met Arg Gln Glu Val Ser Phe Gly
221 225      230      235      240
223 Lys Leu Lys Leu Thr Asn Asn Lys Gly Ala Ser Asn Asn Val Thr Gln
224      245      250      255
226 Met Ile Val Leu Gln Ser Leu His Lys Tyr Gln Pro Arg Leu His Ile
227      260      265      270
229 Val Glu Val Asn Asp Gly Glu Pro Glu Ala Ala Cys Asn Ala Ser Asn
230      275      280      285
232 Thr His Ile Phe Thr Phe Gln Glu Thr Gln Phe Ile Ala Val Thr Ala
233      290      295      300
235 Tyr Gln Asn Ala Glu Ile Thr Gln Leu Lys Ile Asp Asn Asn Pro Phe
236 305      310      315      320
238 Ala Lys Gly Phe Arg Glu Asn Phe Glu Ser Met Tyr Thr Ser Val Asp
239      325      330      335
241 Thr Ser Ile Pro Ser Pro Pro Gly Pro Asn Cys Gln Phe Leu Gly Gly
242      340      345      350
245 Asp His Tyr Ser Pro Leu Leu Pro Asn Gln Tyr Pro Val Pro Ser Arg
246      355      360      365
248 Phe Tyr Pro Asp Leu Pro Gly Gln Ala Lys Asp Val Val Pro Gln Ala
249      370      375      380
251 Tyr Trp Leu Gly Ala Pro Arg Asp His Ser Tyr Glu Ala Glu Phe Arg
252 385      390      395      400
254 Ala Val Ser Met Lys Pro Ala Phe Leu Pro Ser Ala Pro Gly Pro Thr
255      405      410      415
257 Met Ser Tyr Tyr Arg Gly Gln Glu Val Leu Ala Pro Gly Ala Gly Trp
258      420      425      430
260 Pro Val Ala Pro Gln Tyr Pro Pro Lys Met Gly Pro Ala Ser Trp Phe
261      435      440      445
263 Arg Pro Met Arg Thr Leu Pro Met Glu Pro Gly Pro Gly Gly Ser Glu
264      450      455      460
266 Gly Arg Gly Pro Glu Asp Gln Gly Pro Pro Leu Val Trp Thr Glu Ile
267 465      470      475      480
269 Ala Pro Ile Arg Pro Glu Ser Ser Asp Ser Gly Leu Gly Glu Gly Asp
270      485      490      495
272 Ser Lys Arg Arg Arg Val Ser Pro Tyr Pro Ser Ser Gly Asp Ser Ser

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Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\07292005\J008264B.raw

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273          500          505          510
275 Ser Pro Ala Gly Ala Pro Ser Pro Phe Asp Lys Glu Ala Glu Gly Gln
276          515          520          525
278 Phe Tyr Asn Tyr Phe Pro Asn
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283 <211> LENGTH: 1593
284 <212> TYPE: DNA
285 <213> ORGANISM: Mus musculus
287 <220> FEATURE:
288 <221> NAME/KEY: CDS
289 <222> LOCATION: (1)..(1590)
291 <400> SEQUENCE: 3
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294 1 5 10 15
296 ccg atg ccg agt gac gag ggc cgg ggg ccc gga gcg gac caa cag cat 96
297 Pro Met Pro Ser Asp Glu Gly Arg Gly Pro Gly Ala Asp Gln Gln His
298 20 25 30
300 cgt ttc ttc tat ccc gag ccg ggc gca cag gac ccg acc gat cgc cgc 144
301 Arg Phe Phe Tyr Pro Glu Pro Gly Ala Gln Asp Pro Thr Asp Arg Arg
302 35 40 45
306 gca ggt agc agc ctg ggg acg ccc tac tct ggg ggc gcc ctg gtg cct 192
307 Ala Gly Ser Ser Leu Gly Thr Pro Tyr Ser Gly Gly Ala Leu Val Pro
308 50 55 60
310 gcc gcg ccg ggt cgc ttc ctt gga tcc ttc gcc tac ccg ccc cgg gct 240
311 Ala Ala Pro Gly Arg Phe Leu Gly Ser Phe Ala Tyr Pro Pro Arg Ala
312 65 70 75 80
314 cag gtg gct ggc ttt ccc ggg cct ggc gag ttc ttc ccg ccg ccc gcg 288
315 Gln Val Ala Gly Phe Pro Gly Pro Gly Glu Phe Phe Pro Pro Pro Ala
316 85 90 95
318 ggt gcg gag ggc tac ccg ccc gtg gat ggc tac cct gcc cct gac ccg 336
319 Gly Ala Glu Gly Tyr Pro Pro Val Asp Gly Tyr Pro Ala Pro Asp Pro
320 100 105 110
322 cgc gcg ggg ctc tac cca ggg ccg cgc gag gac tac gca ttg ccc gcg 384
323 Arg Ala Gly Leu Tyr Pro Gly Pro Arg Glu Asp Tyr Ala Leu Pro Ala
324 115 120 125
326 ggg ttg gag gtg tct ggg aag ctg aga gtc gcg ctc agc aac cac ctg 432
327 Gly Leu Glu Val Ser Gly Lys Leu Arg Val Ala Leu Ser Asn His Leu
328 130 135 140
330 ttg tgg tcc aag ttc aac cag cac cag aca gag atg atc atc act aag 480
331 Leu Trp Ser Lys Phe Asn Gln His Gln Thr Glu Met Ile Ile Thr Lys
332 145 150 155 160
334 caa gga ccg cga atg ttc cca ttc ctg tcc ttc acc gtg gcc ggg ctg 528
335 Gln Gly Arg Arg Met Phe Pro Phe Leu Ser Phe Thr Val Ala Gly Leu
336 165 170 175
338 gag ccc aca agc cat tac agg atg ttt gtg gat gtg gtc ttg gtg gac 576
339 Glu Pro Thr Ser His Tyr Arg Met Phe Val Asp Val Val Leu Val Asp
340 180 185 190

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needs explanation in <2207-22237
section

<210> 5

<211> 27

<212> DNA

<213> Artificial Sequence

see p. 7 for error explanation

<400> 5

gggaatttca cacctaggtg aaattcc

27

<210> 6

<211> 24

<212> DNA

<213> Artificial Sequence

<400> 6

aatttcacac ctaggtgtga aatt

24

<210> 7

<211> 24

<212> DNA

<213> Artificial Sequence

<400> 7

gagctatcac ctaagtgtgg gcta

24

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

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<210> 9

<211> 24

<212> DNA

<213> Artificial Sequence

<400> 9

aaactgctgt ctaaacaatgg gcta

24

Attorney Docket No.: HUI-040CP

10

delete

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/008,264B

DATE: 07/29/2005
TIME: 08:03:59

Input Set : A:\SEQUENCE LISTING.txt
Output Set: N:\CRF4\07292005\J008264B.raw

error explanation

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

Seq#: 5, 6, 7, 8, 9

VERIFICATION SUMMARY

DATE: 07/29/2005

PATENT APPLICATION: US/10/008,264B

TIME: 08:03:59

Input Set : A:\SEQUENCE LISTING.txt

Output Set: N:\CRF4\07292005\J008264B.raw

L:546 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
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L:546 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:546 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:546
L:555 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:555 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:555 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:555
L:563 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:563 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:563 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:563
L:571 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
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L:571 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:571 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:571
L:580 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:580 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:580 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:580
L:584 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4
L:585 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9